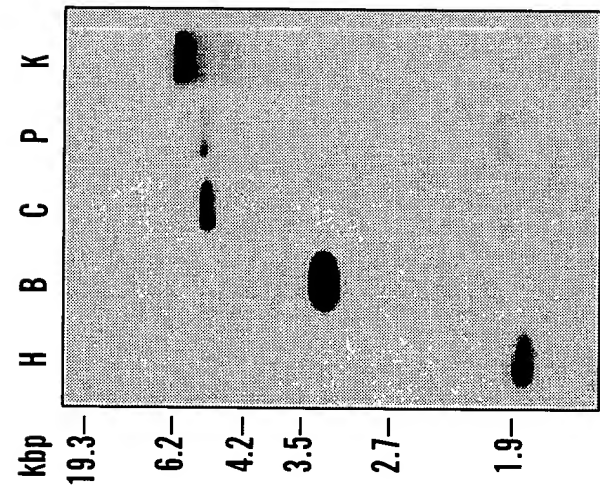
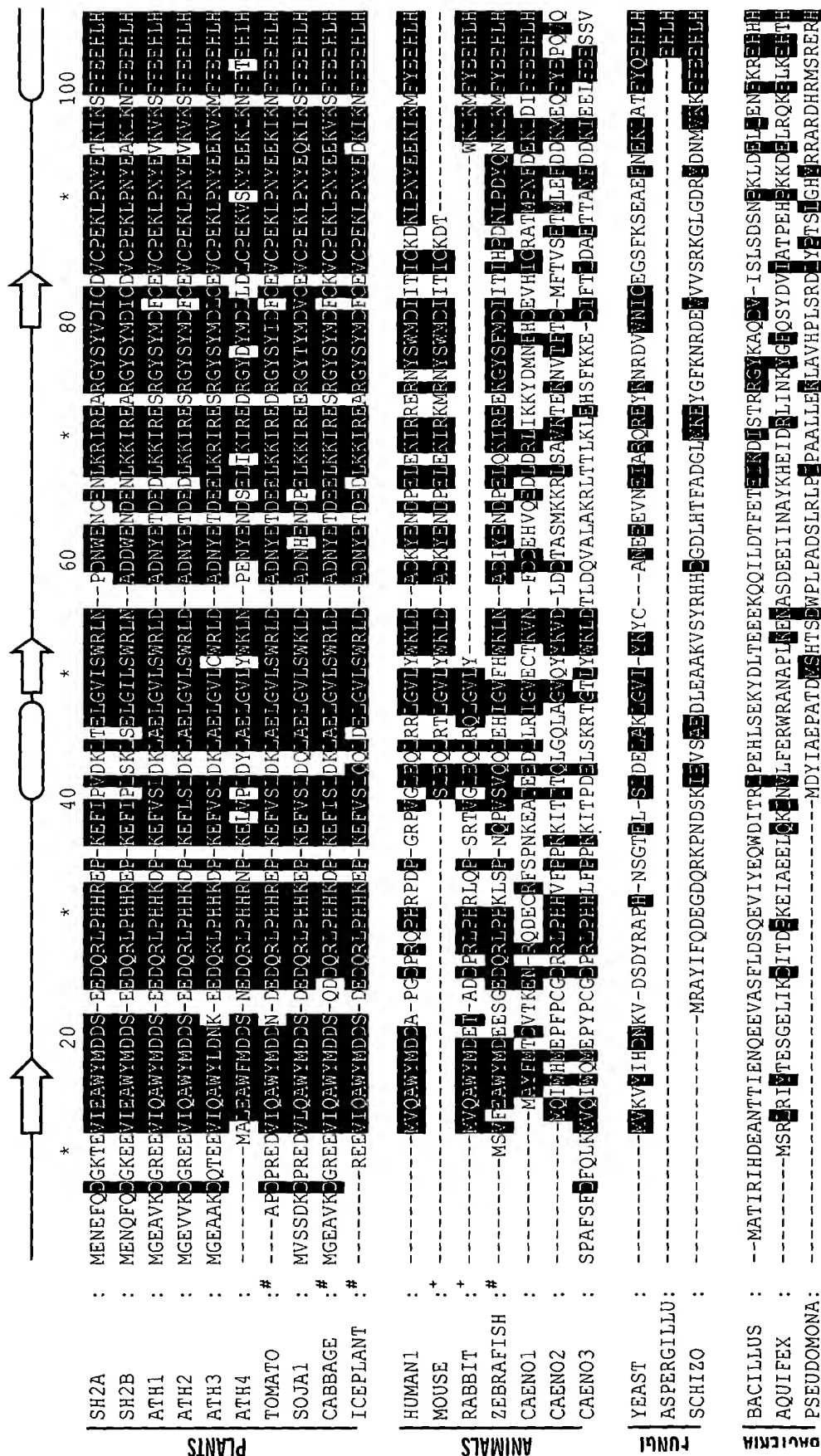


**FIG. 1A**



**FIG. 1B**

**FIG. 1C**



**FIG. 2B**

PLANTS

ANIMALS

FUNGI

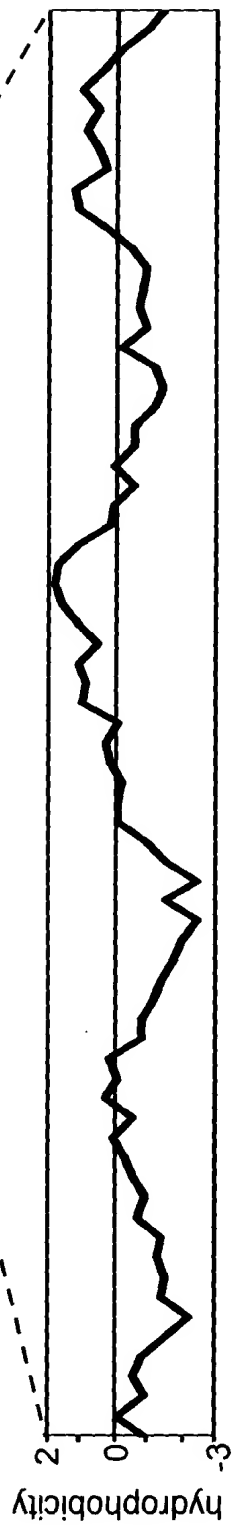
BACTERIA

SH2A	:	TDE	EIRYCLGSGYFVDRDQNDQ	--	MIR	A	MKGGMIVLPAGIYHREFTLDT	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 199
SH2B	:	TDE	EIRYCLGSGYFVDRDQNDQ	--	MIR	AMKGGMIVLPAGIYHREFTLDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 197	
ATH1	:	TDE	EIRYCVAGTGYFVDRDRXEA	--	MIR	VMKGGMIVLPAGIYHREFTVDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 198	
ATH2	:	TDE	EIRYCVAGSGYFVDRDRXEA	--	MIR	VMKGGMIVLPAGIYHREFTVDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 199	
ATH3	:	TDE	EIRYCLAGSGYFVDRDLILI	--	MIR	AMKGGMIVLPAGIYHREFTLDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 199	
ATH4	:	KDE	EIRYCLAGSGYFVDRDQNDQ	--	MIR	AMKGGMIVLPAGIYHREFTLDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 186	
TOMATO	:	#	EIRYAMAGSGYFVDRDMES	--	MIR	AMKGGMIVLPAGIYHREFTLDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 195	
SOJA1	:	TDE	EIRFCAGSGYFVDRDRXEA	--	MIR	VMKGGMIVLPAGIYHREFTLDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 200	
CABBAGE	:	#	EIRYCVAGSGYFVDR	--	MIR	AMKGGMIVLPAGIYHREFTLDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 118	
ICEPLANT	:	#	EIRYCVRSWQAL	--	MIR	AMKGGMIVLPAGIYHREFTLDS	--	DVYIKAMKRLFVGPVWTPYNNRPHDH	--	LPARKKEFLAMLKSEGENQAVEGF*	: 108	
HUMAN1	:	LJD	EIRIILDSGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 179	
MOUSE	:	*	IRIILDSGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 132	
RABBIT	:	*	EIRIILDSGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 137	
ZEBRAFISH	:	#	EIRIILDSGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 116	
CAEN01	:	DJA	EIRVIKHGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 178	
CAEN02	:	KED	VISLWEGTGYDYDEPEDUS	--	MIR	QVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 159	
CAEN03	:	PFE	QVRCGDMITLPAGIYHREFTVDEK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 221	
YEAST	:	EDE	EIRYCLGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 179	
ASPERGILLU	:	#	EIRIIRDSGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 99	
SCHIZO	:	EDE	EIRIILDSGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 178	
BACILLUS	:	TDD	EIRIILDSGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 178	
AQUIFEX	:	SDF	EIRYFVYEDGSGYFVDRDREK	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	--	FEERQVQVXKFLAQTA*	: 181	
PSEUDOMONA	:	DEHI	LTCSECGLLRWR	--	EGBA	--	MIR	IFVRCGDMITLPAGIYHREFTVDEK	--	SNVYIKAMKRLFVGPVWTPYNNRPHDH	: 164	

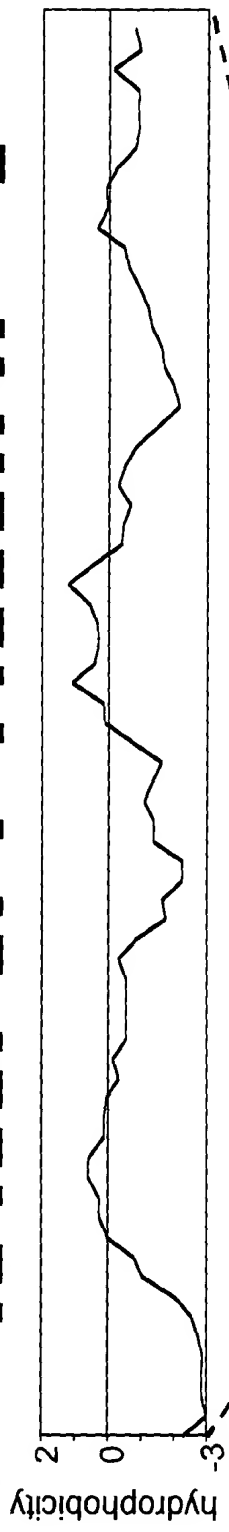
**FIG. 3**

	SH2A	SH2B	ATH1	ATH2	ATH3	ATH4	HUMAN	CAENO1	CAENO2	CAENO3	SCHIZO	SCEREV	BACSUB	AQUIFEX	PSEUDO
<i>Oryza sativa</i> SH2A		84 (93)	70 (85)	71 (87)	67 (83)	59 (74)	50 (67)	30 (49)	20 (35)	23 (46)	33 (46)	32 (51)	17 (33)	14 (29)	14 (24)
<i>Oryza sativa</i> SH2B		84 (93)	75 (87)	75 (88)	70 (84)	60 (75)	54 (69)	31 (49)	20 (35)	24 (47)	31 (44)	33 (50)	18 (33)	14 (29)	14 (24)
<i>Arabidopsis thaliana</i> 1		70 (85)	75 (87)		92 (95)	80 (88)	57 (73)	32 (52)	20 (36)	26 (47)	33 (45)	35 (51)	18 (34)	14 (30)	14 (26)
<i>Arabidopsis thaliana</i> 2		71 (87)	75 (88)	92 (95)		82 (89)	58 (75)	31 (50)	18 (34)	24 (45)	33 (46)	34 (50)	18 (33)	14 (30)	13 (25)
<i>Arabidopsis thaliana</i> 3		67 (83)	70 (84)	80 (88)	82 (89)		57 (73)	30 (50)	18 (34)	23 (45)	23 (45)	33 (48)	18 (32)	15 (30)	12 (26)
<i>Arabidopsis thaliana</i> 4		59 (74)	60 (75)	57 (73)	58 (75)	57 (73)	54 (70)	34 (53)	23 (46)	24 (41)	27 (41)	39 (56)	19 (32)	18 (30)	12 (24)
<i>Homo sapiens</i>		50 (67)	54 (69)	56 (69)	54 (68)	54 (69)	54 (70)	39 (58)	22 (37)	29 (53)	35 (51)	38 (55)	19 (34)	17 (32)	12 (23)
<i>Caenorhabditis elegans</i> 1		30 (49)	31 (49)	32 (52)	31 (50)	30 (50)	34 (53)	39 (58)	15 (29)	23 (46)	36 (51)	32 (49)	18 (35)	20 (33)	11 (25)
<i>Caenorhabditis elegans</i> 2		20 (35)	20 (35)	20 (36)	18 (34)	18 (34)	23 (46)	22 (37)	15 (29)	33 (48)	15 (29)	15 (31)	10 (23)	9 (20)	5 (12)
<i>Caenorhabditis elegans</i> 3		23 (46)	24 (47)	26 (47)	24 (45)	23 (45)	24 (41)	29 (53)	23 (46)	33 (48)	22 (42)	21 (45)	14 (35)	12 (25)	8 (22)
<i>Schizosaccharomyces pombe</i>		33 (46)	31 (44)	33 (45)	33 (46)	33 (48)	27 (41)	35 (51)	15 (29)	22 (42)		37 (58)	18 (36)	20 (34)	14 (26)
<i>Saccharomyces cerevisiae</i>		32 (51)	33 (50)	35 (51)	34 (50)	34 (50)	39 (56)	38 (55)	15 (31)	21 (45)	37 (58)		16 (33)	17 (30)	15 (24)
<i>Bacillus subtilis</i>		17 (33)	18 (33)	18 (34)	18 (33)	18 (32)	19 (32)	18 (35)	10 (23)	14 (35)	18 (36)	16 (33)		26 (46)	6 (19)
<i>Aquifex aeolicus</i>		14 (29)	14 (29)	14 (30)	14 (30)	15 (30)	18 (30)	20 (33)	9 (20)	12 (25)	20 (34)	17 (30)	26 (46)		7 (19)
<i>Pseudomonas aeruginosa</i>		14 (24)	14 (24)	14 (26)	13 (25)	12 (26)	12 (23)	11 (25)	5 (12)	8 (22)	14 (26)	15 (24)	6 (19)	7 (19)	
	SH2A	SH2B	ATH1	ATH2	ATH3	ATH4	HUMAN	CAENO1	CAENO2	CAENO3	SCHIZO	SCEREV	BACSUB	AQUIFEX	PSEUDO

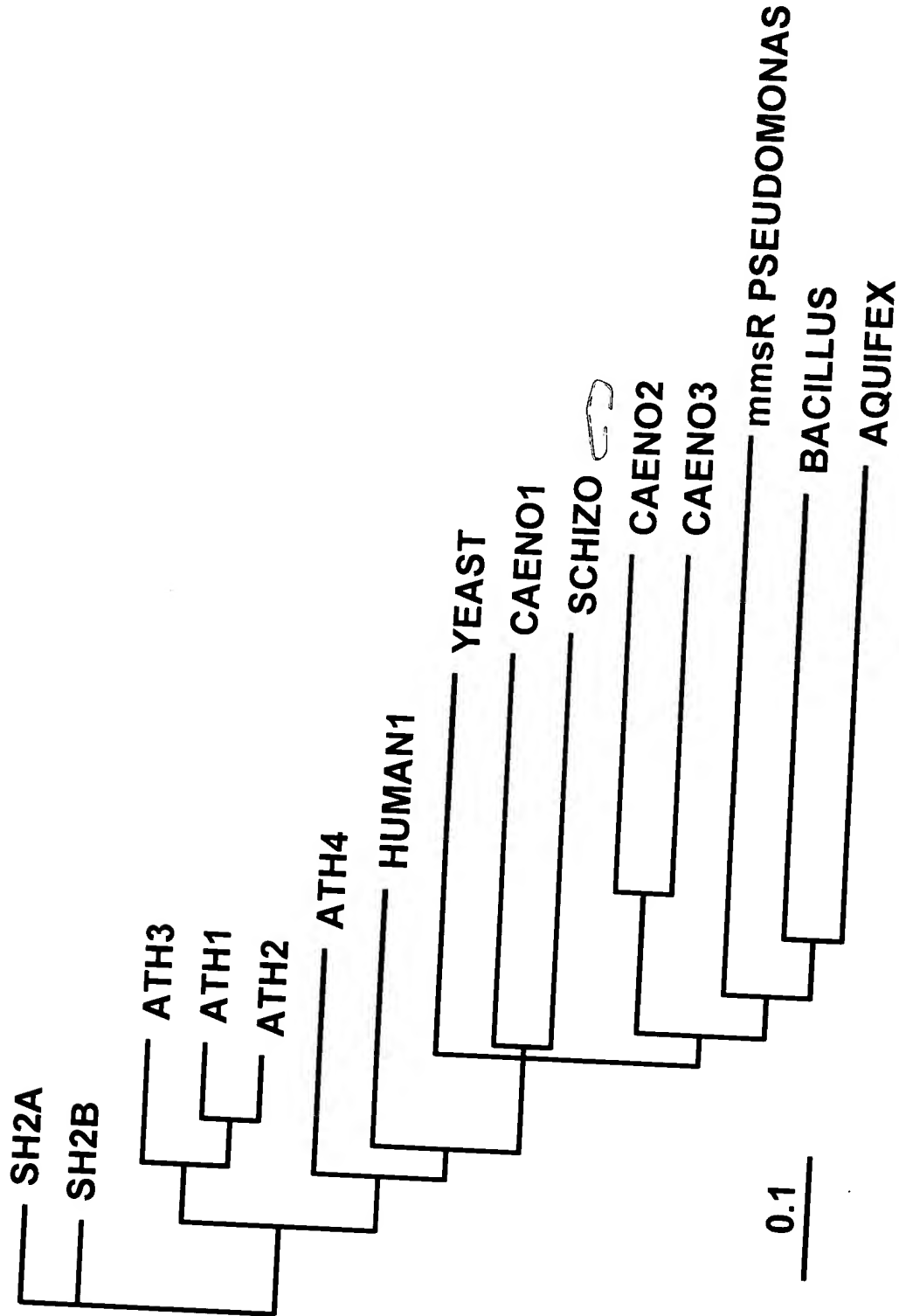
**FIG. 4**



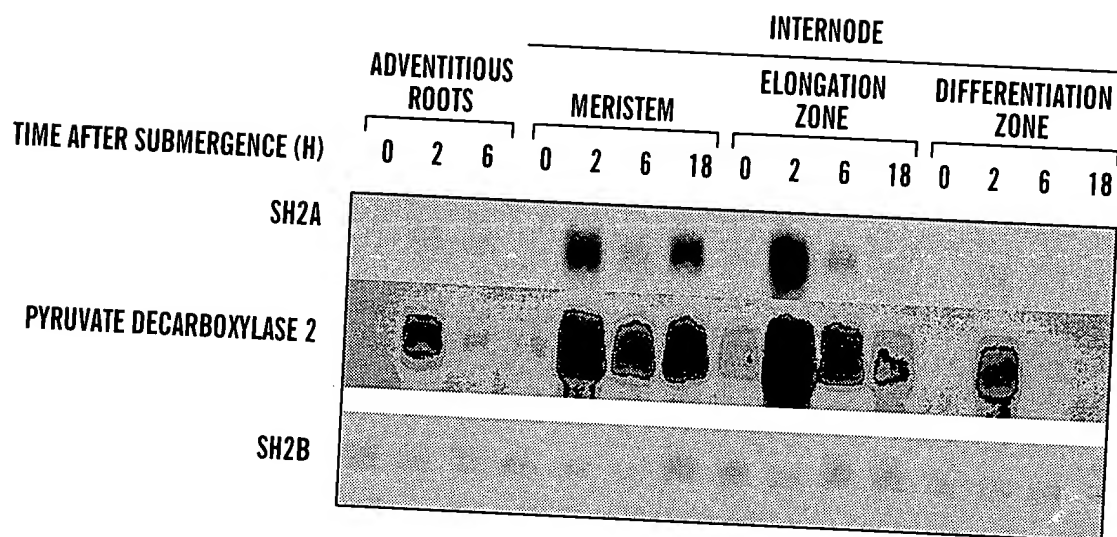
95 FFEHHTDE-FIRYCLEGSGYFDVRDQNDQWIRIALKKGGMIVLHPAGMYHRTLTDTNLIKAMRLFVGDPVWT. 167  
 60 RMSRERH-DEHLLIYCSEGQGLLRVR-EGEAWREYRVGSGDLLWLPFGMAHDYAAD-DRQPWT--IFWTHLRGD\* 131



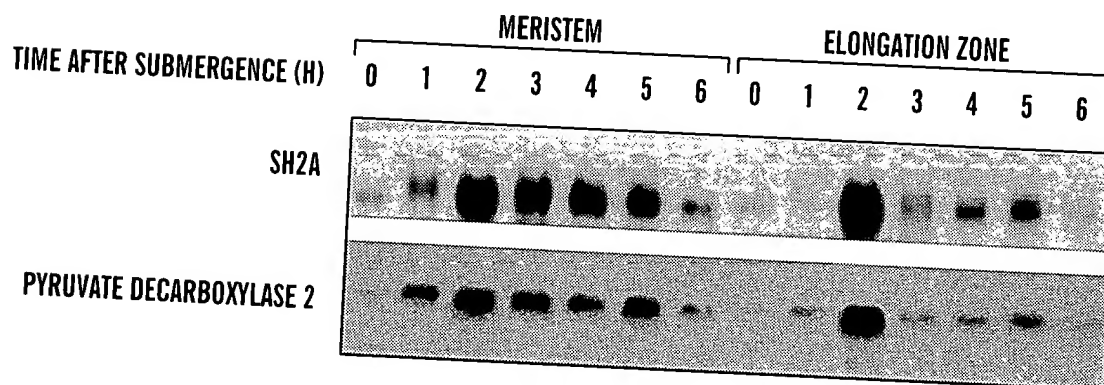
nonconserved region  
 conserved domain  
 DNA-binding

**FIG. 5**

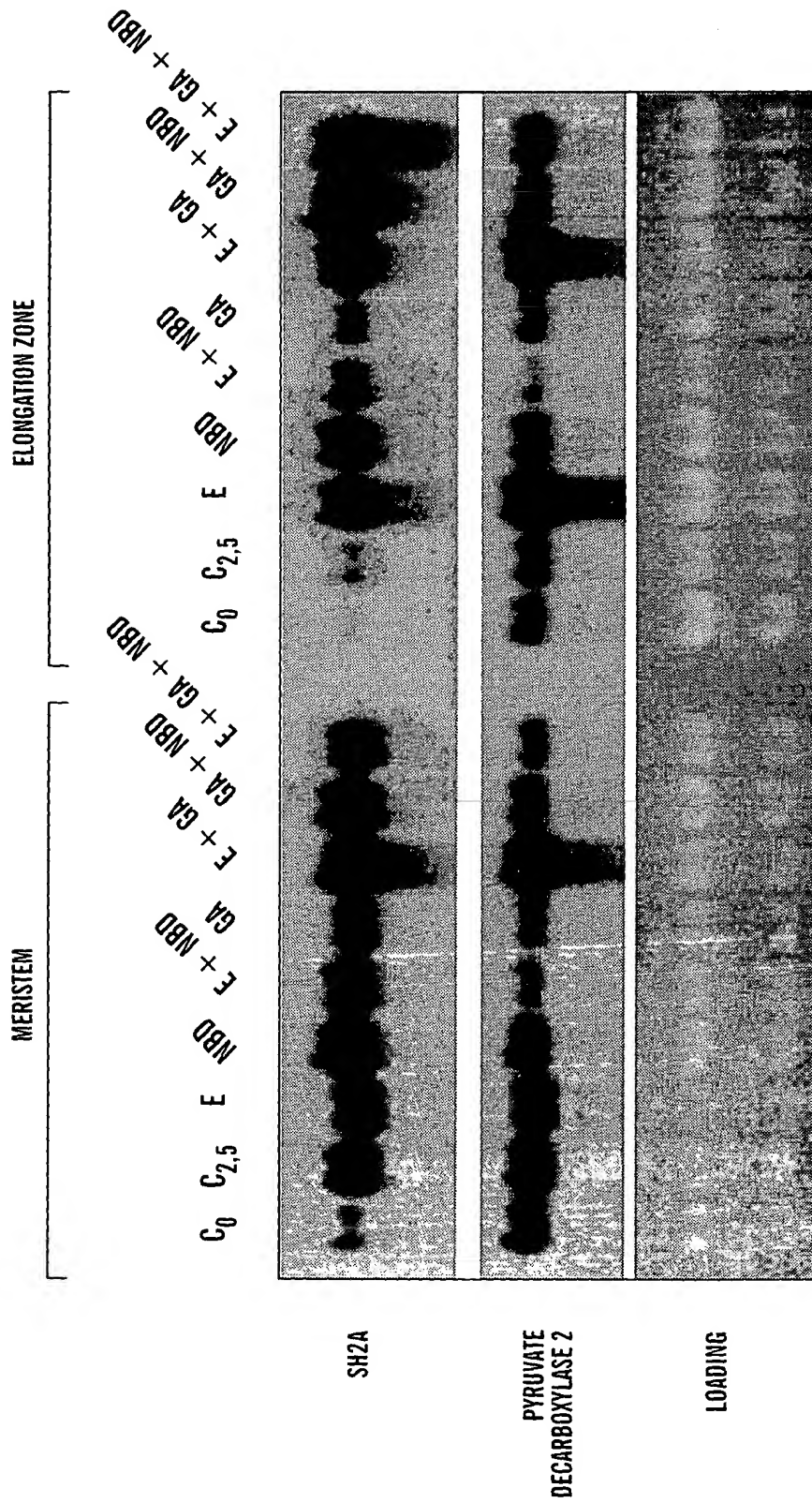
7/11



**FIG. 6A**



**FIG. 6B**



**FIG. 7**



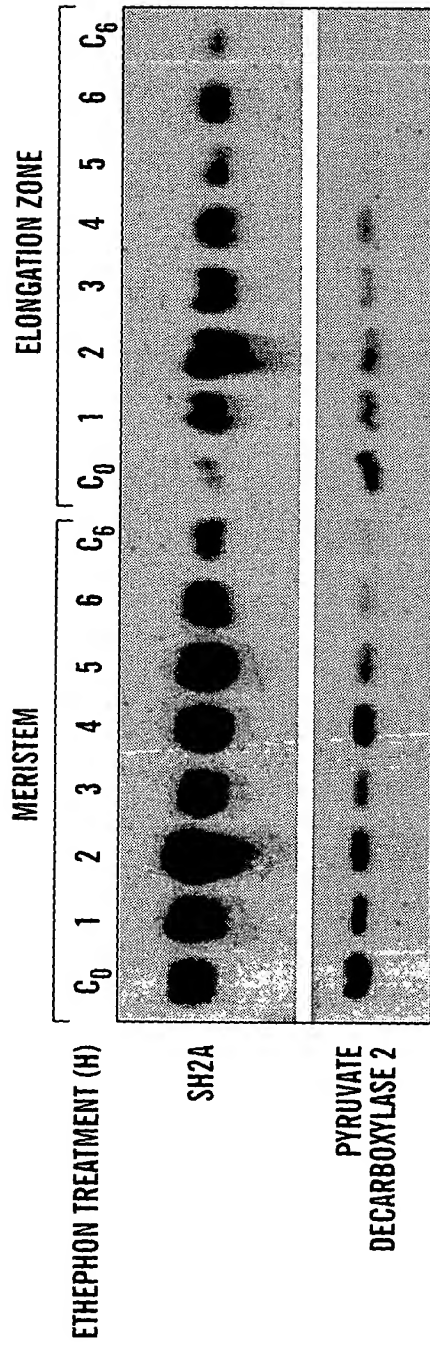


FIG. 8A

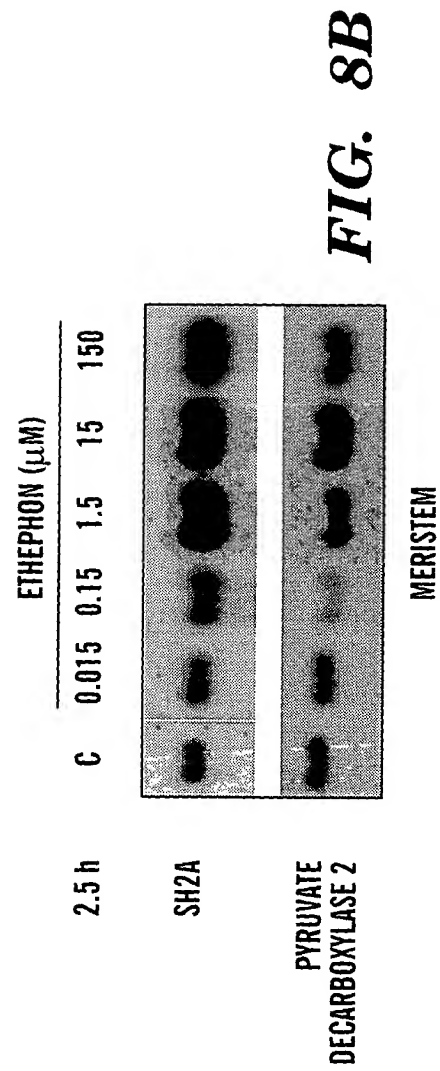
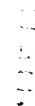


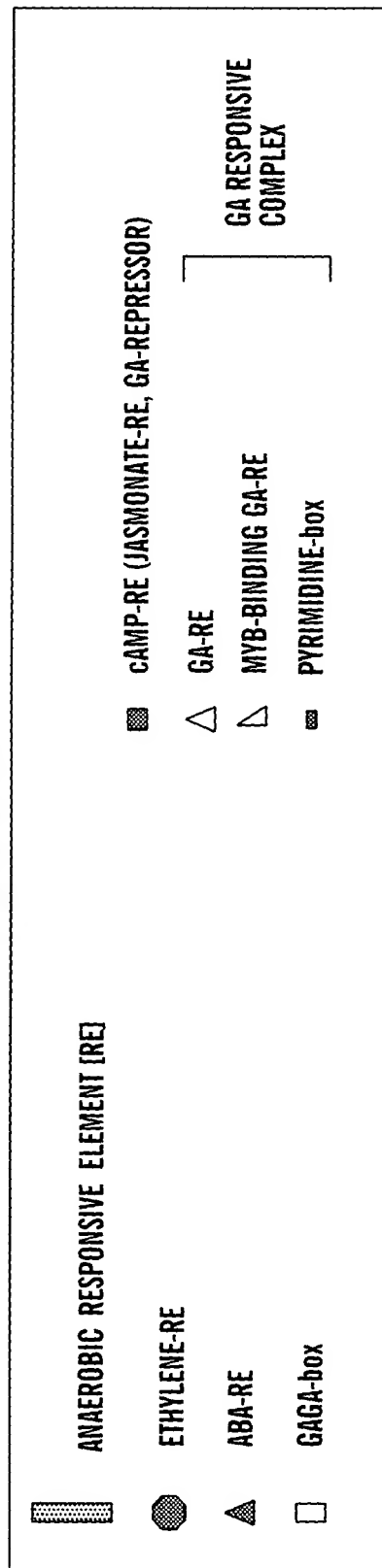
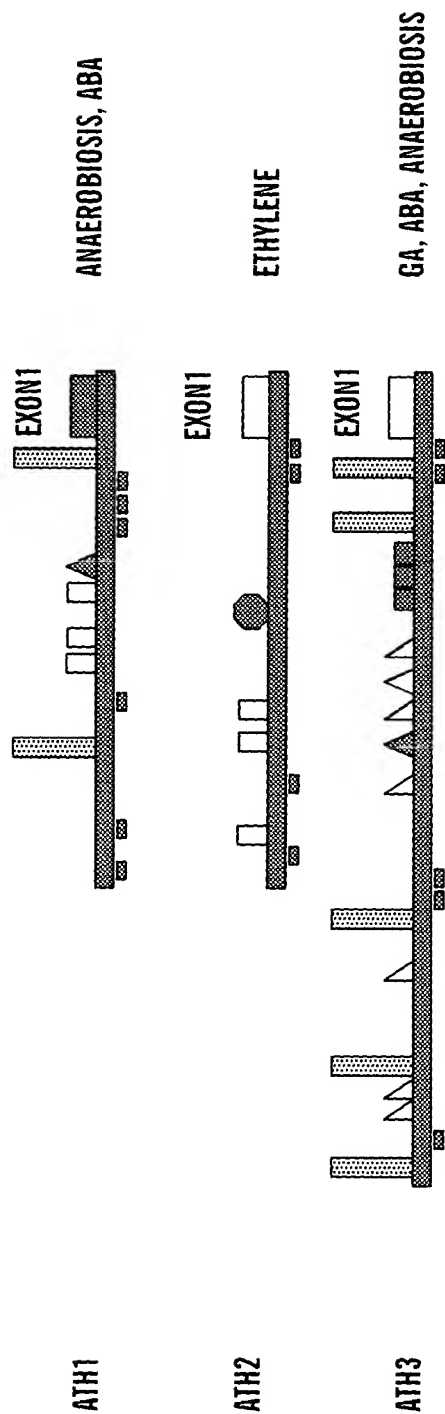
FIG. 8B

2



1

PUTATIVE REGULATORY SIGNALS



**FIG. 10**